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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/776,874A

DATE: 12/12/2001
TIME: 11:51:23

Input Set : A:\ES.txt
Output Set: N:\CRF3\12112001\I776874A.raw

ENTERED

3 <110> APPLICANT: Pecker, Iris
 4 Vlodavsky, Israel
 5 Feinstein, Elena
 7 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE
 ACTIVITY AND
 8 EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
 10 <130> FILE REFERENCE: 01/22603
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/776,874A
 C--> 12 <141> CURRENT FILING DATE: 2001-12-12
 12 <150> PRIOR APPLICATION NUMBER: US 08/922,170
 13 <151> PRIOR FILING DATE: 1997-09-02
 15 <150> PRIOR APPLICATION NUMBER: US 09/109,386
 16 <151> PRIOR FILING DATE: 1998-07-10
 18 <150> PRIOR APPLICATION NUMBER: PCT/US98/17954
 19 <151> PRIOR FILING DATE: 1998-08-31
 21 <160> NUMBER OF SEQ ID NOS: 47
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 27
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Artificial sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: synthetic oligonucleotide
 33 <400> SEQUENCE: 1
 34 ccatccta at acgactcact ataggc 27
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 24
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Artificial sequence
 42 <220> FEATURE:
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 49 <210> SEQ ID NO: 3
 50 <211> LENGTH: 23
 51 <212> TYPE: DNA
 52 <213> ORGANISM: Artificial sequence
 54 <220> FEATURE:
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 58 actcaactata gggctcgagc ggc 23
 61 <210> SEQ ID NO: 4
 62 <211> LENGTH: 22
 63 <212> TYPE: DNA
 64 <213> ORGANISM: Artificial sequence
 66 <220> FEATURE:
 67 <223> OTHER INFORMATION: synthetic oligonucleotide
 69 <400> SEQUENCE: 4

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22

70 gcatcttagc cgtcttctt cg
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75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial sequence
78 <220> FEATURE:
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85 <210> SEQ ID NO: 6
86 <211> LENGTH: 23
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial sequence

90 <220> FEATURE:
91 <223> OTHER INFORMATION: synthetic oligonucleotide

93 <400> SEQUENCE: 6 23

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98 <211> LENGTH: 24
99 <212> TYPE: DNA

100 <213> ORGANISM: Artificial sequence

102 <220> FEATURE:
103 <223> OTHER INFORMATION: synthetic oligonucleotide

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109 <210> SEQ ID NO: 8

110 <211> LENGTH: 9

111 <212> TYPE: PRT

112 <213> ORGANISM: Homo sapiens

114 <400> SEQUENCE: 8

116 Tyr Gly Pro Asp Val Gly Gln Pro Arg

117 1 5

120 <210> SEQ ID NO: 9

121 <211> LENGTH: 1721

122 <212> TYPE: DNA

123 <213> ORGANISM: Homo sapiens

125 <400> SEQUENCE: 9 60

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128 agatgctgct ggcgtcgaaag cctgcgtgc cgccgcgcgt gatgctgctg ctcctggggc 180

130 cgctgggtcc cctctccctt ggcgcctgc cccgacactgc gcaagcacag gacgtcgtag 240

132 acctggactt cttcacccag gagccgtgc acctggtag cccctcgatc ctgtccgtca 300

134 ccattgacgc caacctggcc acggacccgc gtttcctcat cctcctgggt tctccaaagc 360

136 ttcgtacattt ggccagaggc ttgtctctg cgtacactgag gtttggggc accaagacag 420

138 acttcctaattttgcgttcc aagaaggaat caaccttga agagagaat tactggcaat 480

140 ctcaagtcaa ccaggatatt tgcaaataatg gatccatccc tcctgtatgtg gaggagaat 540

142 tacggttgga atggccctac caggagcaat tgctactccg agaacactac cagaaaaat 600

144 tcaagaacag cacctactca agaagctctg tagatgtgct atacactttt gcaaactgct 660

146 caggactgga ttgtatctt ggcctaaatg cggttattaaag aacagcagat ttgcagtgg 720

148 acagttctaa tgctcagttg ctcctggact actgctctc caagggat aacatttctt

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150	gggaactagg	caatgaacct	aacagttcc	ttaagaaggc	tgatatttc	atcaatgggt	780
152	cgcagtagg	agaagattat	attcaattgc	ataaaacttct	aagaaagtcc	accttcaaaa	840
154	atgcaaaact	ctatggcct	gatgttggc	agcctcgaag	aaagacggct	aagatgctga	900
156	agagcttcct	gaaggcttgt	ggagaagtga	ttgattcagt	tacatggcat	cactactatt	960
158	tgaatggacg	gactgctacc	aggaaagatt	ttctaaaccc	tgatgtattg	gacattttt	1020
160	tttcatctgt	gcaaaaagg	ttccaggtgg	ttgagagcac	caggcctggc	aagaaggct	1080
162	ggttaggaga	aacaagctct	gcataatggag	gcggagcgcc	cttgctatcc	gacaccttt	1140
164	cagctggctt	tatgtggctg	gataaattgg	gcctgtcagc	ccgaatggga	atagaagtgg	1200
166	tgatgaggca	agtattctt	ggagcagggaa	actaccattt	agtggatgaa	aacttcgatc	1260
168	cttacactga	ttattggcta	tctcttctgt	tcaagaaatt	ggtgggcacc	aaggtgttaa	1320
170	tggcaagcgt	gcaagggtca	aagagaagga	agcttcgagt	atacttcat	tgcacaaaca	1380
172	ctgacaatcc	aaggtataaa	gaaggagatt	taactctgta	tgccataaac	ctccataacg	1440
174	tcaccaagta	cttgcggta	ccctatccct	tttctaaca	gcaagtggat	aaataccctc	1500
176	taagacctt	gggacctcat	ggattactt	ccaaatctgt	ccaactcaat	ggtctaactc	1560
178	taaagatggt	ggatgatcaa	accttgcac	ctttaatgga	aaaacctctc	cggccaggaa	1620
180	gttcactgg	cttgcagct	ttctcatata	gttttttgt	gataagaaat	gccaaagtt	1680
182	ctgcttgcat	ctgaaaataa	aatatactag	tcctgacact	g		1721

187 <210> SEQ ID NO: 10

188 <211> LENGTH: 543

189 <212> TYPE: PRT

190 <213> ORGANISM: Homo sapiens

192 <400> SEQUENCE: 10

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195	1					5				10				15			
198	Leu	Leu	Gly	Pro	Leu	Gly	Pro	Leu	Ser	Pro	Gly	Ala	Leu	Pro	Arg	Pro	
199						20				25				30			
202	Ala	Gln	Ala	Gln	Asp	Val	Val	Asp	Leu	Asp	Phe	Phe	Thr	Gln	Glu	Pro	
203						35				40				45			
206	Leu	His	Leu	Val	Ser	Pro	Ser	Phe	Leu	Ser	Val	Thr	Ile	Asp	Ala	Asn	
207						50				55				60			
210	Leu	Ala	Thr	Asp	Pro	Arg	Phe	Leu	Ile	Leu	Leu	Gly	Ser	Pro	Lys	Leu	
211						65				70				75			80
214	Arg	Thr	Leu	Ala	Arg	Gly	Leu	Ser	Pro	Ala	Tyr	Leu	Arg	Phe	Gly	Gly	
215						85				90				95			
218	Thr	Lys	Thr	Asp	Phe	Leu	Ile	Phe	Asp	Pro	Lys	Lys	Glu	Ser	Thr	Phe	
219						100				105				110			
222	Glu	Glu	Arg	Ser	Tyr	Trp	Gln	Ser	Gln	Val	Asn	Gln	Asp	Ile	Cys	Lys	
223						115				120				125			
226	Tyr	Gly	Ser	Ile	Pro	Pro	Asp	Val	Glu	Glu	Lys	Leu	Arg	Leu	Glu	Trp	
227						130				135				140			
230	Pro	Tyr	Gln	Glu	Gln	Leu	Leu	Leu	Arg	Glu	His	Tyr	Gln	Lys	Phe		
231						145				150				155			160
234	Lys	Asn	Ser	Thr	Tyr	Ser	Arg	Ser	Ser	Val	Asp	Val	Leu	Tyr	Thr	Phe	
235						165				170				175			
238	Ala	Asn	Cys	Ser	Gly	Leu	Asp	Leu	Ile	Phe	Gly	Leu	Asn	Ala	Leu	Leu	
239						180				185				190			
242	Arg	Thr	Ala	Asp	Leu	Gln	Trp	Asn	Ser	Ser	Asn	Ala	Gln	Leu	Leu	Leu	
243						195				200				205			
246	Asp	Tyr	Cys	Ser	Ser	Lys	Gly	Tyr	Asn	Ile	Ser	Trp	Glu	Leu	Gly	Asn	

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247	210	215	220
250	Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser		
251	225	230	235
254	Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser		240
255	245	250	255
258	Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg		
259	260	265	270
262	Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu		
263	275	280	285
266	Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr		
267	290	295	300
270	Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile		
271	305	310	315
274	Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly		320
275	325	330	335
278	Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Ala		
279	340	345	350
282	Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys		
283	355	360	365
286	Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val		
287	370	375	380
290	Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro		
291	385	390	395
294	Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr		400
295	405	410	415
298	Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg		
299	420	425	430
302	Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly		
303	435	440	445
306	Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu		
307	450	455	460
310	Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu		
311	465	470	475
314	480	485	495
315	Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met		
318	500	505	510
319	515	520	525
322	Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser		
323	530	535	540
326	Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile		
327	530	535	540
330	<210> SEQ ID NO: 11		
331	<211> LENGTH: 1721		
332	<212> TYPE: DNA		
333	<213> ORGANISM: Homo sapiens		
335	<220> FEATURE:		
336	<221> NAME/KEY: CDS		
337	<222> LOCATION: (63)..(1691)		
338	<223> OTHER INFORMATION:		

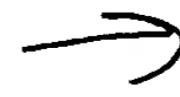
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344 ag atg ctg ctg cgc tcg aag cct gcg ctg ccg ccg ctg atg ctg	107		
345 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu			
346 1 5 10 15			
348 ctg ctc ctg ggg ccg ctg ggt ccc ctc tcc cct ggc gcc ctg ccc cga	155		
349 Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg			
350 20 25 30			
352 cct gcg caa gca cag gac gtc gtg gac ctg gac ttc ttc acc cag gag	203		
353 Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu			
354 35 40 45			
356 ccg ctg cac ctg gtg agc ccc tcg ttc ctg tcc gtc acc att gac gcc	251		
357 Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala			
358 50 55 60			
360 aac ctg gcc acg gac ccg ttc ctc atc ctc ctg ggt tct cca aag	299		
361 Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys			
362 65 70 75			
364 ctt cgt acc ttg gcc aga ggc ttg tct cct gcg tac ctg agg ttt ggt	347		
365 Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly			
366 80 85 90 95			
368 ggc acc aag aca gac ttc cta att ttc gat ccc aag aag gaa tca acc	395		
369 Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Ser Thr			
370 100 105 110			
372 ttt gaa gag aga agt tac tgg caa tct caa gtc aac cag gat att tgc	443		
373 Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys			
374 115 120 125			
376 aaa tat gga tcc atc cct gat gtg gag gag aag tta cgg ttg gaa	491		
377 Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu			
378 130 135 140			
380 tgg ccc tac cag gag caa ttg cta ctc cga gaa cac tac cag aaa aag	539		
381 Trp Pro Tyr Gln Glu Gln Leu Leu Arg Glu His Tyr Gln Lys Lys			
382 145 150 155			
384 ttc aag aac agc acc tac tca aga agc tct gta gat gtg cta tac act	587		
385 Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr			
386 160 165 170 175			
388 ttt gca aac tgc tca gga ctg gac ttg atc ttt ggc cta aat gcg tta	635		
389 Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu			
390 180 185 190			
392 tta aga aca gca gat ttg cag tgg aac agt tct aat gct cag ttg ctc	683		
393 Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu			
394 195 200 205			
396 ctg gac tac tgc tct tcc aag ggg tat aac att tct tgg gaa cta ggc	731		
397 Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly			
398 210 215 220			
400 aat gaa cct aac agt ttc ctt aag aag gct gat att ttc atc aat ggg	779		
401 Asn Glu Pro Asn Ser Phe Leu Lys Ala Asp Ile Phe Ile Asn Gly			
402 225 230 235			
404 tcg cag tta gga gaa gat tat att caa ttg cat aaa ctt cta aga aag	827		
405 Ser Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys			

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.



VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:3199 M:341 W: (46) "n" or "xaa" used, for SEQ ID#:47